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RAW SEQUENCE LISTING

DATE: 05/14/2002

PATENT APPLICATION: US/10/038,937

TIME: 15:00:19

Input Set : N:\Crf3\RULE60\10038937.txt
Output Set: N:\CRF3\05142002\J038937.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Daggett, Lorrie P.
                            Lu, Chin-Chun
      6
            (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
      9
     10
                                     SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
           (iii) NUMBER OF SEQUENCES: 63
     12
            (iv) CORRESPONDENCE ADDRESS:
     14
                  (A) ADDRESSEE: Heller Ehrman White & McAuliffe
     15
                  (B) STREET: 4250 Executive Square, 7th Floor
     16
     17
                  (C) CITY: La Jolla
     18
                  (D) STATE: CA
                  (E) COUNTRY: U.S.A.
     19
                                                                  ENTERED
     20
                  (F) ZIP: 92037
     22
             (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Floppy disk
                  (B) COMPUTER: IBM PC compatible
     24
     25
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     26
     28
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/10/038,937
C--> 29
C-->30
                  (B) FILING DATE: 18-Apr-2002
     45
                  (C) CLASSIFICATION:
     42
           (vii) PRIOR APPLICATION DATA:
                  (A) APPLICATION NUMBER: 08/935,105
     33
                  (B) FILING DATE: 29-SEPT-97
     34
                  (A) APPLICATION NUMBER: US 08/231,193
     38
                  (B) FILING DATE: 20-APR-1994
     39
                  (A) APPLICATION NUMBER: US 08/052,449
     4.3
     44
                  (B) FILING DATE: 20-APR-1993
     47
          (viii) ATTORNEY/AGENT INFORMATION:
     48
                  (A) NAME: Seidman, Stephanie
     49
                  (B) REGISTRATION NUMBER: 33,779
     50
                  (C) PEFERENCE/DOCKET NUMBER: 6362-9383D
     52
            (ix) TELECOMMUNICATION INFOFMATION:
                  (A) TELEPHONE: 619-238-0999
     53
                  (B) TELEFAX: 619-238-0062
     54
        (2) INFORMATION FOR SEQ ID NO: 1:
     57
     59
             (i) SEQUENCE CHARACTERISTICS:
     60
                  (A) LENGTH: 4298 base pairs
     61
                  (B) TYPE: nucleic acid
     62
                  (C) STRANDEDNESS: both
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(D) TOPOLOGY: both

6.3

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65 (ii) MOLECULE TYPE: cDNA													
68 (ix) FEATURE:													
69 (A) NAME/KEY: CDS													
70 (B) LOCATION: 2623078													
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	60												
74 CAAGCCGGGC GIICGGAGCI GIGCCCGGCC CCGCIICAGC ACCGCGGACA GCGCCGGCCG 76 CGIGGGGCTG AGCGCCGAGC CCCCGCGCAC GCIICAGCCC CCCIICCCTC GGCCGACGIC	120												
78 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180												
80 GGACGGCCG GAAGCCCGC GGGGGATGCG CCGAGGGCCC CGCGTICGCG CCGCGCAGAG	240												
82 CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291												
83 Met Ser Thr Met Arg Leu Leu Thr Leu Ala	251												
84 1 5 10													
86 CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339												
87 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile													
88 15 20 25													
90 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387												
91 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe													
92 30 35 40													
94 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG AFT	435												
95 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile													
96 45 50 55													
98 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483												
99 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met													
100 60 65 70	E 2.1												
102 GCT CTG TCG GIG TGC GAG GAC CTC ATC TCC AGC CAG GTC IAC GCC ATC	531												
103 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 104 75 80 85 90													
104 75 80 85 90 106 CTA GTT AGC CAI CCA CCI ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579												
107 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Ihr Pro	3/3												
108 95 100 105													
110 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627												
111 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr													
112 110 115 120													
114 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675												
115 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu													
116 125 130 135													
118 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723												
119 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met													
120 140 145 150													
122 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771												
123 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp													
124 155 160 165 170													
126 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819												
127 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu													
128 175 180 185	967												
130 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867												
131 Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 132 190 195 200													
	915												
134 AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	713												

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	Asn	Val		Ala	Leu	Leu	Met		Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
136			205	T 2 T			~	210	a		202	N. 27	215	T. G	-2.70	2.21	0.63
													GTA				963
	116		Leu	Ser	ALA	Ser		Asp	Asp	Ala	Ala		Val	lyr	Arg	Ala	
140		22:)		2.50			225	200	T. G. G.	2.2.2		230	T-3-3	.3.7.3	.3.5.3	2.2.2	1 (1 1
													TGG				1011
		Ala	Met	Leu	Asn		Inr	GIA	Ser	GLY		vaı	Гrр	Leu	vai		
	235					240		200	ama	2.2.2	245		221			250	1050
													CCA				1059
	GLU	Arg	GLU	rre		GLY	Asn	Ala	Leu	-	ıyr	Ala	Pro	Asp		rre	
149	2.5.2	202	200	~. ~	255			220		260	22.2	F 2 2	2.2.2		265	1.3.3	1107
													GCC				1107
	Leu	GIY	Leu		Leu	116	Asn	GIA	_	Asn	GIU	Ser	Ala		He	ser	
153	~ . ~	202	3(0.3	270	200.2	27.2	2.2.2	212	275	ama	21.2	23.2	ara	280	בי א בי	22.7	1155
													CTC				1155
	ASP	Ala		ЭΙУ	VdI	Val	ALa		Ala	Val	HIS	15 1 11	Leu	Leu	GIU	LYS	
157		220	285	1.00			222	290	000	m.a.a	ביתוב.		295	۲, ٦,٦	A A (7	A T. (7	1203
													AAC				1203
	GIU	300	116	1111	ASP	PLO	305	AIG	GTÅ	CYS	val	310	Asn	1111	ASII	TIE	
161	ביבית		A (7)(7)	בובובו	ביריבי	ביתיר.		አአሮ	A C A	יי די בי	יישיי.		TCT	Tirir	אאר	тлт	1251
													Ser				1231
	315	гуз	1111	אדני	FII	320	FIIC	пуз	nry	Val	325	Mec	251	3021	цуз	330	
		ТΔЭ	aga	ата	Δαπ		cec	GTG	GAG	ጥጥሮ		GAG	GAT	ccc	GAC		1299
													Asp				12,5
169	n.r.u	пэр	OL Y	vai	335	JII	1119	vai	014	340	11511	51 a	1100	321	345	9	
	AAG	TTC	GCC	AAC		AGC	ATC	ATG	AAC		CAG	AAC	CGC	AAG		GTG	1347
													Arg				
173	-1-			350	. 1				355					360			
	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AA'T	GAC	AGG	AAG	1395
176	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	
177			365		-		-	370					375	_	-	-	
179	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443
180	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	
181		380					385					390					
183	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491
184	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	
185	395					400					405					410	
187	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539
188	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	
189					415					420					425		
													CCC				1587
192	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	
193				430					435					440			
													TGC				1635
	ser	Pro	_	Ser	Pro	Arg	His		Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	
197			445					450					455				
													AAC				1683
200	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	

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201		460					465					470					
2013	GAG	GTG	CAC	CIG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
204	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
	475					480					485					490	
207	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CIG	CIC	1779
208	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
2019					495					500					505		
														AAC			1827
212	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	He	Asn	Asn	Glu	
-13				510					515					520			
														CAG			1875
216	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Гуr	Gln	Gly	Leu	
217			525					530					535				
														GAC			1923
220	Thr	Ile	Leu	Val	Lys	Lys		Ile	Pro	Arg	Ser		Leu	Asp	Ser	Phe	
221		540					545					550					
														CTG			1971
		Gln	Pro	Phe	Gln		Thr	Leu	Trp	Leu		Val	Gly	Leu	Ser		
	555					560					565		_			570	
														AGC			2019
	His	Val	Val	Ala		Met	Leu	Tyr	Leu		Asp	Arg	Phe	Ser		Phe	
229					575					580					585		
														GCA			2067
	Gly	Arg	Phe	_	Val	Asn	Ser	GIu		GLu	GLu	Glu	Asp	Ala	Leu	Inr	
233	~ ~			590			m m a		595	000		-3750	.am.a	600	m.a.a	70.7	.115
														AAC			2115
	Leu	ser		Ala	мет	rrp	Pne		Trp	GIY	vai	Leu		Asn	261	(a I Y	
237	A TO CO		605	200	200	ביביבי	A C A	610	TO TO CO	TOA	,,,,,,	aca	615	ome.	(2,2,2	٨٣٦	2163
														CTG Leu			103
	rre	620	Ju	(3 T.A.	Ald	PIO	625	ser	Phe	ser	ALG	630	116	Leu	13 T Å	мес	
241	/am/a		ביריבי	מממ	முரும்	בובובו		እ ሞ <i>ር</i>	λTC	CTC	בובובו		тас	ACC	בורובו	۸۸۵	2211
														Thr			2211
	635	пр	ніа	ary	PHE	640	Mec	116	116	vai	645	261	ı yı	1111	AIU	650	
		GCG	cee	בידיד	ста		СТС	GAC	ccc	ccc		GAG	cgc	ATC	ACG		2259
														Ile			2233
249	Lea	AIG	nia	riic	655	val	ьса	МЭР	nr 9	660	0.1.1	·) .L u	1119	11.5	665	311	
	ATC	A A (*	CAC	ССТ		стс	AGG	AAC	CCC		GAC	AAG	TTT	ATC		GCC	2307
														Ile			
253														680			
														CAG		GAG	2355
														Gln			
257			685	0111	001	201		690		-1-		,	695				
	CTG	AGC		ATG	TAC	CGG	CAT		GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
														Glu			
261		700			1 -	- 9	705			4		710	_				
	GCG		GCC	ATC	CAG	GCC		AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
														Ala			
265						720		_	=		725					730	

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267 TOGG GAC TOG GCG GTG CTG GAG TTC GAG GCC TOG CAG AAU TGC GAC CTG 268 TTP ASP SER ALA VAI LEU GIU PHE GLU ALA SER JIN LYS CYS ASP LEU 269 735 740 745 271 GTG AGG AGG GAG CTG ITI ITC CGC TOG GGC ITC GCG ATG GCC ATG 272 VAI THR THR GLY GLU LEU PHE PHE ATG SER GLY PHE GLY ILE GLY MET 273 750 755 750 760 275 CGC AAA GAC AGC CCC TGG AAG CAG CTG TCC CTG TCC ATG CTC AAG 276 CAR GAL SAP SER PRO TTP LYS GLN ANN VAI SER LEU SER ITE LEU LYS 277 705 279 FCC CAC GAG AAT GGC TTC ATG GAA GAC GTG GCC GTG GCC ATG CTC AAG 280 SER HIS GLU ASN GLY PHE MET GLU ASP LEU ASP LYS THR ITP VAI ATG 281 TAT CAG GAA TGT GAC CCC GCC AGC AAC GCC CTG GCA CAC CTT ACT ITT 284 TYR GLN GAL GCC GCC GCC AGC AAC GCC CTG GCA CAC CTT ACT ITT 287 TYR GAA ACA CAG GCC TTC ATG CTG GAT ACT ACT CTC 288 GLU ASN MET ALG GCY GCC AGC AAC GCC CTA GCC ACC CTT ACT TTC 287 TAG ACC ACC ACC CTT CATG CTG GAT ACC ACC GCC ACC CTT ACT TTC 288 GLU ASN MET ALG GCY GCG GCC ACC CTT ACT CTC 289 BLU ASN MET ALG GCY GCG GCC ACC CTT ACT TTC 280 BLU ASN MET ALG GCY GCG GCC ACC CTT ACT CTC 291 GLY ILE PHE LEU ILE PHE ILE GLU ILE ALG TYR LYS ATG HIS LYS ASP 293 830 815 820 825 294 GLY TCC CTG ATT TCC ATC GAG ATT GCC TAC AAG GCC CAC CAC 295 GCT CGC CGG AAG CAG ATG CAG GCC TTT GCC GCC GTT ACC TTC 296 GLY ILE PHE LEU ILE PHE ILE GLU ILE ALG TYR LYS ATG HIS LYS ASP 297 BLY AGG ACC CTG CAG GAT AGA AAG ACG ATG GTG GCC 288 GLU AGA CAG ATG GAG GCG ACC GCC ACC CTG GCC 288 GLU AGA CAG ATG CAG GCT GCC TTT GCC GCC GTT ACC GCC 297 BLY ACC ACC AGC AAG CAG ATG GAG GCC ACC GCC ACC ACC ACC ACC ACC AC																		
745																		2499
271 GIG ACG ACT GGA GAG CTG TTT ITC CGC TCG GGC TTC GGC ATA GGC ATG CTC 272 Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Tte Gly Met 750 750 750 755 760 760 755 760 760 755 760 760 760 760 760 760 760 760 760 760	268	Trp	Asp	Ser	Ala		Leu	Glu	Phe	Glu		Ser	Gln	Lys	$C_I^{\alpha}S$	-	Leu	
272 Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Tle Gly Met 273 750																		
275																		2547
275 CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG FCC ATC CTC AAG CTC ATC ATC CTC ATC CTC ATC ATC ATC CTC ATC ATC		Val	Thr	Thr	_	Glu	Leu	Phe	Phe		Ser	Gly	Phe	Gly		Gly	Met	
276 Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 775 765 770 775																		
277 765 770 775 776 775 279 765 2643 2840 2840 287 816 2841 284																		2595
279 TOC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG CGG		Arg	Lys	_	Ser	Pro	Trp	Lys		Asn	Val	Ser	Leu		Ile	Leu	Lys	
280 Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Ihr Irp Val Arg	_																	
281 780 785 790 283 TAT CAG GAA TGI GAC TCG CGC AGC AGC CGC GC CCT GCG ACC CTT ACI TTT 2691 284 TYY GIN Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 810 805 800 805 810 810 2739 287 GAG AAC ATG GCC GGG GTC TIC ATG CTG GTA GGT GGG GGG ATC GTG GCC 2739 288 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 820 825 825 291 6GG ATC TTC CTG ATT TTC ATG GAG ATT GC TAG AAG CGG CAC AAG GAT 2787 2788 2787 2787 2787 2787 2787 2787 2787 2787																		2643
283 TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT		Ser		Glu	Asn	Gly	Phe		Glu	Asp	Leu	Asp	-	Ihr	Irp	Val	Arg	
284 Tyr Gln Glu Cys Asp Ser Arg Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 85 795 800 805 810 810 2739 810 2739 810 2739 810 2739 810 2739 288 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 889 815 820 825 825 825 825 825 825 825 825 826 825 826 825 826 825 827 830 836 820 825 825 827 827 827 827 827 827 827 827 827 827 828 820 825 827 827 827 827 827 827 827 827 828 820 828 820 828 820 828 820 828 820 828 820 828 820 828 829 828 820 828 820 828 820 828 820 828 820 828 820 828 820 828 <td></td>																		
285 795 800 805 810 2739 2739 288 304 305 30																		2691
287 GAG AAC ATG GCC GGG GTC TFC ATG CTG GTA GCT GGG GGC ATC GTG GCC 2739 288 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 289 825 291 GGG AFC TFC CTG ATT TTC AFC GAG ATT GCC TAC AAG CGG CAC AAG GAT 2787 292 Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Fyr Lys Arg His Lys Asp 835 840 293 830 835 840 295 GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GC GCT AAC AGTG TGG 2835 296 Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 297 845 850 855 299 CGG AAG ACC CTG CAG GAT AGA AAG AGT GGT AGA AGG CCT GAC CCT 2883 300 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 865 870 301 860 865 870 302 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931 303 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931 304 Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 305 875 880 885 890 307 TTC AAG AGG GCT AGG TCC TCC AAA GAC ACG AGG ACG GGG GGT GAC CCC 2979 308 Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg 909 895 900 905 311 GGT GCT FTG CAA AAC CAA AAA GAC ACA GTG CCG CGG CGC GCT ATT 3027 312 Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 313 910 915 313 GAGACTCCC CGCCGCCCC CCTCTCTCCCCC GCG GGCTGGC GGT GAC AGC GCG GTC ATT 3027 314 GGT GCT FTG CAA AAC CAA AAA GAC ACA GTG CTG TGT TCC AGC 3075 315 GAG AGG GAG GAG GCC CAG CTG CAG CTG CTG TGT TCC CGT CAT AGG GAG AGC 3075 316 Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 915 317 GAGACTCCC CGCCGCCCC CCTCTCTCCCCCGCA GAGCCACG GGGTGGC GGTCACCC 3255 325 GTCCCGGCCC CCGGCCCCCC CCTCTCTCCCCCGCA GAGCCACG GGGTTGGC GGTCACCCC 3255 325 GTCCCGGCCC CCGGCCCCCC CCAGCGTGG GGCCAACCGG CGCCTTCTCT GTGTTTCT 3315 327 ATTTTGCAGC GTGTGTGAGG CCCCGGGGGG GGCCCACCTG CCCAGGGTTGC CGCCCCCCCCCC		-	Gln	Glu	Cys	Asp		Arg	Ser	Asn	Ala		Ala	Thr	Leu	Thr		
288 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 289 825 820 825 826 827 826 827 827 828																		
288																		2/39
2787 291 GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT 2787 292 Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 840 845 850 855 85		Glu	Asn	Met	Ala	_	Val	Phe	Met	Leu		Ala	Gly	GLy	He		Ala	
292 Gly Tle Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp																		0707
293 830 835 840 295 GCT CGC CGG AAG CAG ATG CAG CTG GCC GTTT GCC GCC GTT AAC GTG TGG 2835 296 Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 855 297 845 850 855 299 CGG AAG AAC CTG CAG GAT AGA AAG AAG AGT GGT AGA GCA GAG CCT GAC CCT 2883 300 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 861 860 865 870 301 860 865 860 865 870 880 880 880 880 880 890 2931 880 885 890 891 890 890 890 895 890 900 905 890 89																		2/8/
295 GCT CGC CGG AAG CAG ATG CTG GCC FTT GCC GTT AAC GTG TGG 2835 296 Ala Arg Arg Lys GIN Met GIN Leu Ala Phe Ala Ala Val Asn Val Trp 299 CGG AAG AAC CTG CAG GAT AAG AAG AGT GGT AGA AGA GAC CCT 2883 300 Arg Lys Asn Leu GIN Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 301 860 860 865 870 870 880 870 891 895 890 895 890 895 890 895 890 895 890 905 905 311 GGT GGT GAA AAA ACA		GLY	Ile	Phe		He	Phe	He	Glu		Ala	lyr	Lys	Arg		Lys	Asp	
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297 845 850 855 299 CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT 2883 300 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870 301 860 865 870 870 870 303 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC GTG GCT TCC AGC CTG GCT TCC AGC CTG GCT TCC AGC CTG GCT TCC AGC CTG GCT TCC AGC GCT GCT GCT GCT GCT GCT GCT GCT GCT G																		2835
299 CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT CCT 2883 300 Arg Lys Asn Leu Gln Asp Arg Lys Ser GCT ACC CTC ACC CTG GCT TCC AGC 2931 303 AAA AAG AAA GCA ATT AGG GCT ACC CTC ACC CTG ACC ACC CTG AGC ACC		Ala	Arg		Lys	GIn	Met	GIn		Ala	Pue	Ala	Ala		Asn	vaı	ırp	
300 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 301 860 865 870 303 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931 304 Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 890 305 875 880 885 890 307 TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGG ACC GGG GGT GGA CGC 2979 2979 308 Phe Lys Arg Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg 895 900 905 311 GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT 3027 3027 312 Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 915 920 315 GAG AGG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC 3075 3075 316 Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 930 935 317 925 930 935 321 GGACAGCGCC CGGCCCCC CCTCTCTGCCCC CTCCCCGCA GGCTGGGGG AGGACAGA CAGACAGA CAGACAGA CAGACAGA						~- ~									a		aam	2002
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335 CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG 3615																		

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/038,937

DATE: 05/14/2002 TIME: 15:00:20

Input Set : N:\Crf3\RULE60\10038937.txt
Output Set: N:\CRF3\05142002\J038937.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the $\langle 220 \rangle$ to $\langle 223 \rangle$ fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18 Seq#:47; N Pos. 18 Seq#:49; N Pos. 18 Seq#:51; N Pos. 18 Seq#:53; N Pos. 18

Seq#:57; Xaa Pos.1147,1171 Seq#:58; Xaa Pos.1147,1171

VERIFICATION SUMMARY

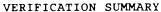
PATENT APPLICATION: US/10/038,937

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

DATE: 05/14/2002 TIME: 15:00:20

Input Set : N:\Crf3\RULE60\10038937.txt
Output Set: N:\CRF3\05142002\J038937.raw

L: 40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:1631 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10 L:2123 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:13 L:2127 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:13 L:2131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2143 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:13 L:2147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:2199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13 L:4013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4021 M:336 W: Invalid Amino Acid Number in Coding Pegion, SEQ ID:23 L:4025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4033 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:23 L:4037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4049 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:23 L:4053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4069 M:336 W: Invalid Amino Acid Number in Coding Pegion, SEQ ID:23 L:4073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4077 M:336 W: Invalid Amino Acid Number in Coding Pegion, SEQ ID:23 L:4081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4097 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:23 L:4101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:4105 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:23 L:4109 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:23



DATE: 05/14/2002 TIME: 15:00:20

PATENT APPLICATION: US/10/038,937

Input Set : N:\Crf3\RULE60\10038937.txt
Output Set: N:\CRF3\05142002\J038937.raw

L:4375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25 L:4379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25 L:4383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25 L:4387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25 L:12994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:57 after pos.:3937 L:13002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:57 after pos.:4033 L:13277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:58 after pos.:1136 L:13283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID:58 after pos.:1168